

10/585620

AP20 Rec'd PCT/PTO 08 JUL 2006

SEQUENCE LISTING

<110> Ye, Liu
Lan, Tang
Spendler, Tina

<120> Amylase

<130> 10583.204-US

<160> 17

<170> PatentIn version 3.3

<210> 1

<211> 1946

<212> DNA

<213> Chaetomium sp.

<220>

<221> CDS

<222> (86)..(1843)

<220>

<221> sig_peptide

<222> (86)..(145)

<220>

<221> mat_peptide

<222> (146)..(1843)

<400> 1

tcccgggtcat cctctcttgg tccctgccat cctcctgccc cctctgatcc accgcctctt	60
cggtggactc caagacgttg tcagg atg cga tcc ttc ctc gcc ctc tca gcc	112
Met Arg Ser Phe Leu Ala Leu Ser Ala	
-20 -15	
ttg ctg ctg ctg tac ccg ctg cag ctg ctc gcc gcc agc aac tcc gac	160
Leu Leu Leu Leu Tyr Pro Leu Gln Leu Leu Ala Ala Ser Asn Ser Asp	
-10 -5 -1 1 5	
tgg agg tcc cgc aat atc tac ttt gcc ttg acc gac cgc gtc gcc aat	208
Trp Arg Ser Arg Asn Ile Tyr Phe Ala Leu Thr Asp Arg Val Ala Asn	
10 15 20	
ccg tcc acc acg acc gca tgt agt gac ctg agc aac tac tgc ggc ggc	256
Pro Ser Thr Thr Thr Ala Cys Ser Asp Leu Ser Asn Tyr Cys Gly Gly	
25 30 35	
acg tgg agc ggc ctg tcg agc aag ctg gac tac atc caa ggg atg ggc	304
Thr Trp Ser Gly Leu Ser Ser Lys Leu Asp Tyr Ile Gln Gly Met Gly	
40 45 50	
ttc gat tcc atc tgg att acc ccc gtg gtc gag aac tgc gac ggt ggc	352
Phe Asp Ser Ile Trp Ile Thr Pro Val Val Glu Asn Cys Asp Gly Gly	

55	60	65	
tac cac ggc tac tgg gcc aag gcg ctc tac aac gtc aac acg aac tac Tyr His Gly Tyr Trp Ala Lys Ala Leu Tyr Asn Val Asn Thr Asn Tyr 70 75 80 85			400
ggc agt gcg gat gat ctg aag aac ttc gtt gcg gcc gcc cat gcg aag Gly Ser Ala Asp Asp Leu Lys Asn Phe Val Ala Ala Ala His Ala Lys 90 95 100			448
ggc atg tac gtg atg gtg gac gtc gtc gcg aat cac atg ggt tcc tgc Gly Met Tyr Val Met Val Asp Val Val Ala Asn His Met Gly Ser Cys 105 110 115			496
ggc atc gcc aac ctc tcc cca cct ccc ctg aac gag cag agc tct tat Gly Ile Ala Asn Leu Ser Pro Pro Pro Leu Asn Glu Gln Ser Ser Tyr 120 125 130			544
cac acc cag tgc gac att gac tac agc agt cag tcc agc att gag acg His Thr Gln Cys Asp Ile Asp Tyr Ser Ser Gln Ser Ser Ile Glu Thr 135 140 145			592
tgc tgg ata tcc ggc ctc cct gac ctg gac acc acc gat agc act atc Cys Trp Ile Ser Gly Leu Pro Asp Leu Asp Thr Thr Asp Ser Thr Ile 150 155 160 165			640
cga tcc ctc ttc cag acc tgg gtc cac ggc ctg gtc agc aac tac agc Arg Ser Leu Phe Gln Thr Trp Val His Gly Leu Val Ser Asn Tyr Ser 170 175 180			688
ttc gac ggt ctc cgc gtc gac acc gtc aag cac gtg gag aag gat tac Phe Asp Gly Leu Arg Val Asp Thr Val Lys His Val Glu Lys Asp Tyr 185 190 195			736
tgg ccc ggc ttc gtg tcg gcg gcg ggc acc tac gcc atc ggc gaa gtc Trp Pro Gly Phe Val Ser Ala Ala Gly Thr Tyr Ala Ile Gly Glu Val 200 205 210			784
ttc tcc ggc gac acc tcc tac gtg gcc ggc tat caa tcg gtg atg ccg Phe Ser Gly Asp Thr Ser Tyr Val Ala Gly Tyr Gln Ser Val Met Pro 215 220 225			832
ggc ttg ctc aac tat ccc atc tac tat ccg ctc atc cgc gtc ttc gcg Gly Leu Leu Asn Tyr Pro Ile Tyr Tyr Pro Leu Ile Arg Val Phe Ala 230 235 240 245			880
cag ggt gcg tcc ttc acc gat ctc gtc aac aac cac gat acc gtc ggc Gln Gly Ala Ser Phe Thr Asp Leu Val Asn Asn His Asp Thr Val Gly 250 255 260			928
tcg acc ttc tcc gac ccg acg ctg ctg ggt aac ttt atc gac aac cac Ser Thr Phe Ser Asp Pro Thr Leu Leu Gly Asn Phe Ile Asp Asn His 265 270 275			976
gac aac cca cgt ttc ctg agc tac acc agc gac cac gcc ctc ctc aag Asp Asn Pro Arg Phe Leu Ser Tyr Thr Ser Asp His Ala Leu Leu Lys 280 285 290			1024

aac gct ctg gcc tac gtc atc ctg gcc aga ggc atc ccc atc gtc tac Asn Ala Leu Ala Tyr Val Ile Leu Ala Arg Gly Ile Pro Ile Val Tyr 295 300 305	1072
tac ggc acc gag caa ggc tac tcg ggt tcg tcc gac ccg gcg aac cgc Tyr Gly Thr Glu Gln Gly Tyr Ser Gly Ser Ser Asp Pro Ala Asn Arg 310 315 320 325	1120
gag gat ctc tgg cgt agc gga tac agc act acg gga gac atc tac acc Glu Asp Leu Trp Arg Ser Gly Tyr Ser Thr Thr Gly Asp Ile Tyr Thr 330 335 340	1168
acc atc gcc gcg ctc tcc gcc gcg cgc acc gcg gcc ggt ggc ctc gcc Thr Ile Ala Ala Leu Ser Ala Ala Arg Thr Ala Ala Gly Gly Leu Ala 345 350 355	1216
ggt aac gac cac gtc cac ctg tac acg acc gac aac gcg tac gcc tgg Gly Asn Asp His Val His Leu Tyr Thr Thr Asp Asn Ala Tyr Ala Trp 360 365 370	1264
tcc cgg gcg agc ggc aag ctc atc gtc gtc acg tcc aac cgc ggc agc Ser Arg Ala Ser Gly Lys Leu Ile Val Val Thr Ser Asn Arg Gly Ser 375 380 385	1312
tcc gac agc agc acc atc tgc ttc agc acc cag cag gcc agc ggc acc Ser Asp Ser Ser Thr Ile Cys Phe Ser Thr Gln Gln Ala Ser Gly Thr 390 395 400 405	1360
acc tgg acc agc acg atc acc ggc aac tcg tac acc gcc gac agc aac Thr Trp Thr Ser Thr Ile Thr Gly Asn Ser Tyr Thr Ala Asp Ser Asn 410 415 420	1408
ggc cag atc tgc gtg cag ctg tcc agc ggc gga ccc gag gcg ctc gtc Gly Gln Ile Cys Val Gln Leu Ser Ser Gly Gly Pro Glu Ala Leu Val 425 430 435	1456
gtc tcc acc gcg acc ggc acc gcc acc gcg acg act ctg tcc acg acc Val Ser Thr Ala Thr Gly Thr Ala Thr Ala Thr Thr Leu Ser Thr Thr 440 445 450	1504
acc aag acg tcc acc tcg acc gcc tcc tgc gcc gcc acc gtc gcc gtc Thr Lys Thr Ser Thr Ser Thr Ala Ser Cys Ala Ala Thr Val Ala Val 455 460 465	1552
acc ttc aac gag ctc gtc acc acg aac tac ggc gac acc atc cgc ctg Thr Phe Asn Glu Leu Val Thr Thr Asn Tyr Gly Asp Thr Ile Arg Leu 470 475 480 485	1600
acg ggc tcc atc tcc cag ctc agc agc tgg agc gca acc tcc ggg ctg Thr Gly Ser Ile Ser Gln Leu Ser Ser Trp Ser Ala Thr Ser Gly Leu 490 495 500	1648
gcc ctg agc gcg tcc gcg tac acg tcc agc aac ccg ctc tgg agc gtg Ala Leu Ser Ala Ser Ala Tyr Thr Ser Ser Asn Pro Leu Trp Ser Val 505 510 515	1696

acg gtc agc ctg ccg gcc ggc acg tcg ttc gag tac aag ttc gtc cgc 1744
 Thr Val Ser Leu Pro Ala Gly Thr Ser Phe Glu Tyr Lys Phe Val Arg
 520 525 530

atc acg agc gac ggc acc gtg acc tgg gaa tcg gac ccg aac cgc agc 1792
 Ile Thr Ser Asp Gly Thr Val Thr Trp Glu Ser Asp Pro Asn Arg Ser
 535 540 545

tac acc gtc ccg acg tgc gcg agc acc gcg acg atc agc aat acc tgg 1840
 Tyr Thr Val Pro Thr Cys Ala Ser Thr Ala Thr Ile Ser Asn Thr Trp
 550 555 560 565

cgg tgagctctgg acgtgttgta catataggag gccgttgaga ggccggggcg 1893
 Arg

gttggtggtc ggggtgaatg gggggttgat gctttttcgt tgtgtcggtg aga 1946

<210> 2
 <211> 586
 <212> PRT
 <213> Chaetomium sp.

<400> 2

Met Arg Ser Phe Leu Ala Leu Ser Ala Leu Leu Leu Tyr Pro Leu
 -20 -15 -10 -5

Gln Leu Leu Ala Ala Ser Asn Ser Asp Trp Arg Ser Arg Asn Ile Tyr
 -1 1 5 10

Phe Ala Leu Thr Asp Arg Val Ala Asn Pro Ser Thr Thr Thr Ala Cys
 15 20 25

Ser Asp Leu Ser Asn Tyr Cys Gly Gly Thr Trp Ser Gly Leu Ser Ser
 30 35 40

Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Asp Ser Ile Trp Ile Thr
 45 50 55 60

Pro Val Val Glu Asn Cys Asp Gly Gly Tyr His Gly Tyr Trp Ala Lys
 65 70 75

Ala Leu Tyr Asn Val Asn Thr Asn Tyr Gly Ser Ala Asp Asp Leu Lys
 80 85 90

Asn Phe Val Ala Ala Ala His Ala Lys Gly Met Tyr Val Met Val Asp
 95 100 105

Val Val Ala Asn His Met Gly Ser Cys Gly Ile Ala Asn Leu Ser Pro
 110 115 120

Pro Pro Leu Asn Glu Gln Ser Ser Tyr His Thr Gln Cys Asp Ile Asp
 125 130 135 140

Tyr Ser Ser Gln Ser Ser Ile Glu Thr Cys Trp Ile Ser Gly Leu Pro
 145 150 155

Asp Leu Asp Thr Thr Asp Ser Thr Ile Arg Ser Leu Phe Gln Thr Trp
 160 165 170

Val His Gly Leu Val Ser Asn Tyr Ser Phe Asp Gly Leu Arg Val Asp
 175 180 185

Thr Val Lys His Val Glu Lys Asp Tyr Trp Pro Gly Phe Val Ser Ala
 190 195 200

Ala Gly Thr Tyr Ala Ile Gly Glu Val Phe Ser Gly Asp Thr Ser Tyr
 205 210 215 220

Val Ala Gly Tyr Gln Ser Val Met Pro Gly Leu Leu Asn Tyr Pro Ile
 225 230 235

Tyr Tyr Pro Leu Ile Arg Val Phe Ala Gln Gly Ala Ser Phe Thr Asp
 240 245 250

Leu Val Asn Asn His Asp Thr Val Gly Ser Thr Phe Ser Asp Pro Thr
 255 260 265

Leu Leu Gly Asn Phe Ile Asp Asn His Asp Asn Pro Arg Phe Leu Ser
 270 275 280

Tyr Thr Ser Asp His Ala Leu Leu Lys Asn Ala Leu Ala Tyr Val Ile
 285 290 295 300

Leu Ala Arg Gly Ile Pro Ile Val Tyr Tyr Gly Thr Glu Gln Gly Tyr
 305 310 315

Ser Gly Ser Ser Asp Pro Ala Asn Arg Glu Asp Leu Trp Arg Ser Gly
 320 325 330

Tyr Ser Thr Thr Gly Asp Ile Tyr Thr Thr Ile Ala Ala Leu Ser Ala
 335 340 345

Ala Arg Thr Ala Ala Gly Gly Leu Ala Gly Asn Asp His Val His Leu
 350 355 360

Tyr Thr Thr Asp Asn Ala Tyr Ala Trp Ser Arg Ala Ser Gly Lys Leu
 365 370 375 380

Ile Val Val Thr Ser Asn Arg Gly Ser Ser Asp Ser Ser Thr Ile Cys
 385 390 395

Phe Ser Thr Gln Gln Ala Ser Gly Thr Thr Trp Thr Ser Thr Ile Thr
 400 405 410

Gly Asn Ser Tyr Thr Ala Asp Ser Asn Gly Gln Ile Cys Val Gln Leu
 415 420 425

Ser Ser Gly Gly Pro Glu Ala Leu Val Val Ser Thr Ala Thr Gly Thr
 430 435 440

Ala Thr Ala Thr Thr Leu Ser Thr Thr Thr Lys Thr Ser Thr Ser Thr
 445 450 455 460

Ala Ser Cys Ala Ala Thr Val Ala Val Thr Phe Asn Glu Leu Val Thr
 465 470 475

Thr Asn Tyr Gly Asp Thr Ile Arg Leu Thr Gly Ser Ile Ser Gln Leu
 480 485 490

Ser Ser Trp Ser Ala Thr Ser Gly Leu Ala Leu Ser Ala Ser Ala Tyr
 495 500 505

Thr Ser Ser Asn Pro Leu Trp Ser Val Thr Val Ser Leu Pro Ala Gly
 510 515 520

Thr Ser Phe Glu Tyr Lys Phe Val Arg Ile Thr Ser Asp Gly Thr Val
 525 530 535 540

Thr Trp Glu Ser Asp Pro Asn Arg Ser Tyr Thr Val Pro Thr Cys Ala
 545 550 555

Ser Thr Ala Thr Ile Ser Asn Thr Trp Arg

560

565

<210> 3
<211> 18
<212> DNA
<213> Artificial

<220>
<223> Primer amyD1

<220>
<221> misc_feature
<222> (3)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (12)..(12)
<223> n is a, c, g, or t

<400> 3
gsntaccayg gntactgg

18

<210> 4
<211> 17
<212> DNA
<213> Artificial

<220>
<223> Primer amyD2R

<220>
<221> misc_feature
<222> (15)..(15)
<223> n is a, c, g, or t

<400> 4
tarayratkg gratncc

17

<210> 5
<211> 17
<212> DNA
<213> Artificial

<220>
<223> Primer AM835n-s1

<220>
<221> misc_feature
<222> (15)..(15)
<223> n is a, c, g, or t

<400> 5
aayaartayt tygcnyt

17

<210> 6
<211> 17
<212> DNA
<213> Artificial

<220>
<223> Primer AM835n-s2a

<220>
<221> misc_feature
<222> (3)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (6)..(6)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (15)..(15)
<223> n is a, c, g, or t

<400> 6
ctnggngaya grgtngc

17

<210> 7
<211> 17
<212> DNA
<213> Artificial

<220>
<223> Primer AM835n-s2b

<220>
<221> misc_feature
<222> (3)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (6)..(6)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (15)..(15)
<223> n is a, c, g, or t

<400> 7
ctnggngayc grgtngc

17

<210> 8
<211> 17
<212> DNA
<213> Artificial

<220>
<223> Primer AM835n-s2c

<220>
<221> misc_feature
<222> (3)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (6)..(6)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (15)..(15)
<223> n is a, c, g, or t

<400> 8
ctnggngayc gygtngc

17

<210> 9
<211> 18
<212> DNA
<213> Artificial

<220>
<223> amy835as1

<400> 9
gcggatagta gatgggat

18

<210> 10
<211> 17
<212> DNA
<213> Artificial

<220>
<223> Primer amy835f2

<400> 10
gtgcgtcctt caccgat

17

<210> 11

<211> 17
<212> DNA
<213> Artificial

<220>
<223> amy835s00

<400> 11
tcccgtcatc ctctctt

17

<210> 12
<211> 18
<212> DNA
<213> Artificial

<220>
<223> amy835as01

<400> 12
tctcaccgac acaacgaa

18

<210> 13
<211> 20
<212> PRT
<213> Chaetomium sp.

<220>
<221> misc_feature
<222> (9)..(9)
<223> Xaa can be any naturally occurring amino acid

<400> 13

Ala Ser Asn Ser Asp Trp Arg Ser Xaa Asn Lys Tyr Phe Ala Leu Gly
1 5 10 15

Asp Arg Val Ala
 20

<210> 14
<211> 17
<212> DNA
<213> Artificial

<220>
<223> amy835as3

<400> 14
gtagtcaatg tcgcact

17

<210> 15

<211> 18
<212> DNA
<213> Artificial

<220>
<223> amy835f1

<400> 15
ccatctacta tccgctca 18

<210> 16
<211> 28
<212> DNA
<213> Artificial

<220>
<223> Primer AM835.1

<400> 16
ccaggatccg tcaggatgcg atccttcc 28

<210> 17
<211> 29
<212> DNA
<213> Artificial

<220>
<223> Primer AM835.2

<400> 17
cgtctcgagg acacaacgaa aaagcatca 29